Remarks

None of the foregoing amendments adds new matter. These amendments are sought to update the priority information for the present application, to correct minor typographical errors in the text, and to bring the text of the specification into conformance with the formal drawings filed herewith, and do not change the scope of the claims. Accordingly, Applicants respectfully request that the foregoing amendments be entered and considered.

In accordance with 37 C.F.R. § 1.821, the computer-readable and paper copies of the sequence listing filed herewith are the same, and contain no new matter.

Summary

It is respectfully believed that this application is now in condition for immediate examination. Early notice to this effect is respectfully requested.

Respectfully submitted,

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Version with markings to show changes made

In the Specification:

Please amend the first full paragraph on page 1 (the Cross Reference section appearing at lines 4-9) as follows:

This application is a divisional of U.S. Application No. 09/019,160, filed February 6, 1998, which claims priority to U.S. Provisional Application No. 60/037,393, filed February 7, 1997, and to [the] U.S. Provisional Application No. 60/037,393, [of Deb K. Chatterjee, Joseph Solus and Shuwei Yang, entitled "Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof,"] filed January 6, 1998, the disclosures of which are fully incorporated herein by reference.

Please amend the fourth full paragraph on page 18 (at lines 14-15) as follows:

FIGURES 10A[and B]-D are composites of a electropherogram gel scan of PCR amplifications at D16S405 and D16S401 loci.

Please amend the fifth full paragraph on page 18 (at lines 16-17) as follows:

FIGURES 11A-B is a composite of a electropherogram gel scan of PCR amplifications at D16S401 locus.

Please amend the sixth full paragraph on page 18 (at lines 18-19) as follows:

FIGURES 12A[and B]-F are composites of a electropherogram gel scan of PCR amplifications at D15S127 and D15S153 loci.

Please amend the seventh full paragraph on page 18 (at lines 20-21) as follows:

FIGURES 13A-C is a composite of a electropherogram gel scan of PCR amplifications at D16S401 locus.

Please amend the second full paragraph on page 86 (at lines 12-22) as follows:

Figure 9 shows two examples of electropherogram gel scans, aligned by PCR product size, comparing the PCR products obtained with *Taq* and *Tne* polymerases with a 10-minute final extension. For the D15S153 locus, *Taq* exhibited non-templated nucleotide addition to 40% of the PCR product (Figure [39]9A), while *Tne* exhibited no such addition of non-templated nucleotides (Figure 9B). Similar results were obtained with the D15S127 locus: 53% of the *Taq* PCR products demonstrated non-templated nucleotide addition (Figure 9C), while none of the *Tne* PCR products demonstrated non-templated nucleotide addition (Figure 9D). These results demonstrate the difficulty in identifying alleles in a heterogeneous pattern as generated by *Taq* amplification, compared to the more homogeneous, simple pattern generated by amplification with *Tne*.

Please amend the second full paragraph on page 87 (at lines 11-21) as follows:

Reactions were loaded into a Perkin Elmer model 9600 thermocycler preheated to 95 °C and PCR was done using recommended cycling conditions (5 min. pre-denaturation at 95°C; 10 cycles of 15 sec at 95°C, 15 sec at 55 °C, and 60 sec at 72 °C; 20 cycles of 15 sec at 89 °C, 15 sec at 55 °C, and 60 sec at 72°C; 10min final extension at 72°C). A portion of each reaction was diluted, mixed with loading cocktail, heat denatured and loaded on [a]an 8% sequencing gel. The ABI 373 Stretch Automated Sequencer was run for 5-6hr at 15W in order to obtain 1base resolution. Data was analyzed using GeneScan software. Areas of the peaks recognized by the software were used to estimate the percent of extranucleotide addition. Table 7 summarizes the results obtained. Examples of the electropherogram data [is]are shown in Figures 10A-D.

Please amend the second full paragraph on page 88 (at lines 11-21) as follows:

Reactions were loaded into a Perkin Elmer model 9600 thermocycler preheated to 95 °C and PCR was done using recommended cycling conditions (5 min. pre-denaturation at 95°C; 10 cycles of 15 sec at 95°C, 15 sec at 55 °C, and 60 sec at 72 °C; 20 cycles of 15 sec at 89 °C, 15 sec at 55 °C, and 60 sec at 72°C; 10min final extension at 72°C). A portion of each reaction was diluted, mixed with loading cocktail, heat denatured and loaded on [a]an 8% sequencing gel. The ABI 373 Stretch Automated Sequencer was run for 5-6hr at

15W in order to obtain 1base resolution. Data was analyzed using GeneScan software. Areas of the peaks recognized by the software were used to estimate the percent of extranucleotide addition. Table 8 summarizes the results obtained. An example of the electropherogram data [is]are shown in Figures 11A-B.

Please amend the second full paragraph on page 90 (at lines 12-22) as follows:

Reactions were loaded into a Perkin Elmer model 9600 thermocycler preheated to 95 °C and PCR was done using recommended cycling conditions (5 min. pre-denaturation at 95°C; 10 cycles of 15 sec at 95 °C, 15 sec at 55 °C, and 60 sec at 72 °C; 20 cycles of 15 sec at 89 °C, 15 sec at 55 °C, and 60 sec at 72 °C; 10min final extension at 72 °C). A portion of each reaction was diluted, mixed with loading cocktail, heat denatured and loaded on [a]an 8% sequencing gel. The ABI 373 Stretch Automated Sequencer was run for 5-6hr at 15W in order to obtain 1base resolution. Data was analyzed using GeneScan software. Areas of the peaks recognized by the software were used to estimate the percent of extranucleotide addition. Table 9 summarizes the results obtained. Examples of the electropherogram data are shown in Figures 12A-F.

Please amend the second full paragraph on page 91 (at lines 15-25) as follows:

Reactions were loaded into a Perkin Elmer model 9600 thermocycler preheated to 95 °C and PCR was done using recommended cycling conditions (5 min. pre-denaturation at 95°C; 10 cycles of 15 sec at 95 °C, 15 sec at 55 °C, and 60 sec at 72 °C; 20 cycles of 15 sec at 89 °C, 15 sec at 55 °C, and 60 sec at 72 °C; 10min final extension at 72 °C). A portion of each reaction was diluted, mixed with loading cocktail, heat denatured and loaded on [a]an 8% sequencing gel. The ABI 373 Stretch Automated Sequencer was run for 5-6hr at 15W in order to obtain 1base resolution. Data was analyzed using GeneScan software. Heights of the n and n+1 peaks recognized by the software were used to estimate the percent of extranucleotide addition. Table 10 summarizes the results obtained. An example of the electropherogram data [is]are shown in Figures 13A-C.